

# BSgenome.Osativa.MSU.MSU7

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BSgenome.Osativa.MSU.MSU7

*Oryza sativa* full genome (MSU7)

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## Description

*Oryza sativa* full genome as provided by MSU (MSU7 Genome Release) and stored in Biostrings objects.

## Note

This BSgenome data package was made from the following source data files:

[ftp://ftp.plantbiology.msu.edu/pub/data/Eukaryotic\\_Projects/o\\_sativa/annotation\\_dbs/pseudomolecu](ftp://ftp.plantbiology.msu.edu/pub/data/Eukaryotic_Projects/o_sativa/annotation_dbs/pseudomolecu)

See [?BSgenomeForge](#) and the BSgenomeForge vignette (`vignette("BSgenomeForge")`) in the BSgenome software package for how to make a BSgenome data package.

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## See Also

[BSgenome-class](#), [DNASTring-class](#), [available.genomes](#), [BSgenomeForge](#)

## Examples

```
BSgenome.Osativa.MSU.MSU7
genome <- BSgenome.Osativa.MSU.MSU7
seqlengths(genome)
genome$Chr1 # same as genome[["Chr1"]]

if ("AGAPS" %in% masknames(genome)) {

  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq)
  {
```

```
## Replace all masks by the inverted AGAPS mask
masks(seq) <- gaps(masks(seq)["AGAPS"])
unique_letters <- uniqueLetters(seq)
if (any(unique_letters != "N"))
  stop("assembly gaps contain more than just Ns")
}

## A message will be printed each time a sequence is removed
## from the cache:
options(verbose=TRUE)

for (seqname in seqnames(genome)) {
  cat("Checking sequence", seqname, "... ")
  seq <- genome[[seqname]]
  checkOnlyNsInGaps(seq)
  cat("OK\n")
}

## See the GenomeSearching vignette in the BSgenome software
## package for some examples of genome-wide motif searching using
## Biostrings and the BSgenome data packages:
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```

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